IN THE SPECIFICATION

Kindly amend the specification as follows.

Page 5, replace the sixth paragraph starting at line 22 with the following:

Figure 3 (a-e) – RNA folds showing predicted secondary structure of SIV_{mac} leader RNA. a) wild type SEQ ID NO:11 b) with Δ1 mutation SEQ ID NO:12 c) with Δ2 mutation SEQ ID NO:13 d) with Δ3 mutation SEQ ID NO:14 e) with Δ4 mutation SEQ ID NO:15. Positions of deletions are shown in a) by arrows and bold type. Shaded areas indicate sequences corresponding to the primer binding site, dimerisation initiation signal and *gag* initiation codon. Thick lines in b), c), d) and e) indicate position of the deleted sequence.

Page 24, replace the first paragraph starting at line 1 with the following:

For Δ1, positions 862-898 (numbering from the start of the 5' U3 sequence, or 171-207 when the first base of the R region is numbered 1) were deleted using the mutagenic oligonucleotide 5' AGTGAGAAGAACTCCACCACGACGGACTGC 3' (SEQ ID NO:3).

Page 24, replace the second paragraph starting at line 4 with the following:

For Δ2, positions 915-947 (or 224-256 on alternative numbering) were deleted using the mutagenic oligonucleotide 5' CCAACCACGACGGAGGCGTGAGGAGCG 3' (SEQ ID NO:4).

Page 24, replace the third paragraph starting at line 7 with the following:

For Δ3, positions 995-1045 (or 304-354 on alternative numbering) were deleted using the mutagenic oligonucleotide 5' CGGTTGCAGGTAAGTGCAAGTGGGAGATGGGC 3' (SEQ ID NO:5).

Page 24, replace the fourth paragraph starting at line 10 with the following:

For Δ4, positions 1011-1042 (or 320-351) were deleted using the mutagenic oligonucleotide 5' GCAACACAAAAAAAGAGTGGGAGATGGGC 3' (SEQ ID NO:6).

Page 24, replace the sixth paragraph starting at line 15 with the following:

Plasmids used as templates for the production of riboprobes were created as follows: SIVKSΨGS used to detect genomic versus spliced RNA was created by amplification of SIV sequences between 818 and 1068 using the primers 5' ATGGGAATTCGTTTCGTTTCTCGCGCCCATCTCCCACTCT 3' (SEQ ID NO:7) and 5'TAATGGATCCAGATTGGCGCCTGAACAGGG 3' (SEQ ID NO:8). The PCR product was then cloned into the *Bam* H1 and *Eco* R1 sites of Bluescript SK + (Stratagene). SIVKSLTR used to discriminate DNA from RNA was created by amplification of SIV sequences between 300 and 750 using the primers 5' CTTTGAATTCACCGAGTACCGAGTTG 3' (SEQ ID NO:9) and 5' TTTGGGATCCTACCCAGAAGAGTTTGG 3' (SEQ ID NO:10) (Figure 2). The PCR product was then cloned into the *Bam* H1 and *Eco* R1 sites of Bluescript SK + (Stratagene).

Page 27, replace the third paragraph starting at line 19 with the following:

We speculated as to whether the Δ4 mutation might have a more profound effect on the secondary structure of the leader RNA and investigated this using the RNA folding programme www(dot)ibc(dot)wustl(dot)edu(backslash)~zuker(backslash)rna(backslash) ~~(www.ibc.wustl.edu/~zuker/rna/)~~. The results are shown in Figure 3 (a-e). Figure 3 shows the RNA structure of the intact region in part a, on which are marked the boundaries of 4 deletion mutants that have been created: at the most extreme 5' end, there is a deletion between the two arrows marked ΔP1; in b, the resulting structure with a bar marks the site of the deleted sequence. The same is true for c for ΔP2 which clearly deletes a structure labelled DIS with some shaded bases (GGUACC) at the tip. Of interest was the fact that the Δ2 mutation which caused the profound packaging defect deletes an RNA stem loop with a palindromic terminus which would be consistent with part of the leader involved in dimerisation and encapsidation. This remains intact in

the Δ1, Δ3 and Δ4 deletions. These deletions did not cause a packaging deletion indicating that the packaging signal has been precisely identified. The Δ4 deletion, however, significantly disrupts the structured region between the putative packaging signal/dimer initiation signal loop and the stem loop containing the viral *gag* initiation codon. Although the Δ3 mutation also disrupts this region, the change in predicted secondary structure is not as severe as that brought about by Δ4 in which a stem loop present in the wild type and other mutants upstream of the Gag initiation codon is replaced by a region of unstructured RNA. We suggest that the dramatic effect of Δ4 may be caused by the severe disruption of secondary structure, possibly affecting *cis* acting functions other than packaging which are dependent on this region.

IN THE SEQUENCE LISTING

Kindly enter the attached Sequence Listing in lieu of the substitute submitted on May 21, 2002.